

**In the Specification:**

Please amend the Paragraph beginning at Page 5, line 18, as follows:

A number of basic residues that are conserved in human, rat, and mouse heparanase are found in proximity to the proposed catalytic proton donor and nucleophile, e.g., KK (residues 231 and 232) near Glu225 and KK (residues 337 and 338) near Glu343. Further, three clusters of basic amino acids that conform to HS-binding protein consensus sequences (xBBBxxBx or xBBxBx) (Cardin, A. D., and Weintraub, H. J. R. *Arteriosclerosis*, 1989 9, 21-32) are present in human heparanase: QKKFKN (residues 157-162) (SEQ ID NO: 12), PRRKTAKM (residues 271-278) (SEQ ID NO: 13) and SKRRKLRV (residues 426-433) (SEQ ID NO: 14). When these conserved residues are mapped onto the structure of endo-1,4-, -xylanase from *P. simplicissimum* (pdb entry 1BG4), three of these four basic clusters (residues 231 and 232, 271-278, and 157-162) can be predicted to be situated on the top of the TIM-barrel fold, in proximity to the proposed active site, potentially interacting with HS. The position of the last basic cluster (residues 426-433) (SEQ ID NO: 14) could not be predicted.